

Amendments to the Specification:

Please delete the current sequence listing and insert the substitute sequence listing after the Abstract.

Please replace the paragraph at page 19, line 37 with the following:

According to preferred aspects of the present invention the compound is a cyclic peptide or analog thereof. Preferably, the compound has the following formula:



wherein X_i is absent or is a peptide of between 1 and 100 amino acids, preferably between about 1 and 50 amino acids, and more preferably between about 1 and 10; X_j is 5 amino acids and X_k is absent or a peptide of between 1 and 100 amino acids, preferably between about 1 and 50 amino acids and more preferably between about 1 and 10, so long as the cyclic peptide or analog thereof retains the qualitative biological activity described above.

Please replace the paragraph at page 21, line 5 with the following:

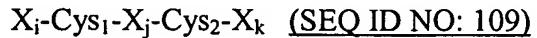
Preferred peptides of the present invention have the following formula:



wherein X_i is absent or is between 1 and 100 amino acids; X_j is 5 amino acids and X_k is absent or between 1 and 100 amino acids. Preferably, X_i and X_k are between 1 and 50 amino acids and more preferably between 1 and 10 amino acids.

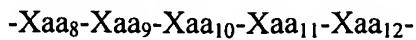
Please replace the paragraph at page 21, line 10 with the following:

By way of exemplification and not limitation, ~~preferred~~ preferred peptides of the present invention include the peptides described in Figure 4. In general, a preferred peptide has the formula:



wherein;

X_j has the formula



and Xaa_8 is an amino acid selected from the group ~~consisting~~ consisting of Trp, Thr, Ala, Phe, Leu, Met and Tyr; Xaa_9 is an amino acid selected from the group consisting of Thr, Asp and Ala;

Xaa₁₀ is an amino acid selected from the group consisting of Trp, Ala, Phe, Leu and Tyr; Xaa₁₁ is an amino acid selected from the group consisting of Glu, Ala, Arg and Gln; and Xaa₁₂ is an amino acid selected from the group consisting of Gly, Asp, Thr, Ser and Ala.

Please replace the paragraph at page 21, lines 23 with the following:

As a further example, preferred peptides have the formula:

Xaa₁- Xaa₂- Xaa₃- Xaa₄- Xaa₅- Xaa₆-Cys- Xaa₈- Xaa₉- Xaa₁₀- Xaa[[1]]₁₁- Xaa[[1]]₁₂-Cys-Xaa₁₄- Xaa₁₅- Xaa₁₆- Xaa₁₇- Xaa₁₈ (SEQ ID NO: 102)

wherein Xaa₁ is any amino acid; Xaa₂ is any amino acid; Xaa₃ is an amino acid selected from the group consisting of Trp, Phe, Leu, Ala, Met and Val; Xaa₄ is an amino acid; Xaa₅ is an amino acid selected from the group consisting of Val, Ile, Ala, Trp and Tyr; Xaa₆ is an amino acid selected from the group consisting of Leu, Ile, Met, Val and Ala; Xaa₈ is selected from the group consisting of Trp, Phe, Leu, Met, Ala and Val; Xaa₉ is an amino acid ; Xaa₁₀ is an amino acid selected from the group consisting of Trp, Phe, Met and Tyr; Xaa₁₁ is any amino acid; Xaa₁₂ is any amino acid; Xaa₁₄ is any amino acid except Pro; Xaa₁₅ is an amino acid selected from the group consisting of Arg, Lys, Leu, Trp, His and Met;

Xaa₁₆ is any amino acid; Xaa₁₇ is any amino acid; and Xaa₁₈ is any amino acid.

Please replace the paragraph at page 40, line 38 with the following:

Phage Libraries - The random sequence polyvalent peptide phage libraries have been described previously (Lowman, H. B., *et al.*, *Biochemistry* 37:8870 (1998)). The peptide libraries were of the form X_iCX_jCX_k (SEQ ID NO:103) (where X was any of the 20 naturally occurring L-amino acids and j ranged from 4-10 and i + j + k=18), an unconstrained library X₂₀ (SEQ ID NO:104), and X₄CX₂GPX₄CX₄ (SEQ ID NO:105). Each of the 10 libraries has in excess of 10⁸ clones.

Please replace the paragraph at page 41, line 1 with the following:

Selection Conditions - TF₁₋₂₄₃ (Paborsky, L. R., *et al.*, *J. Biol. Chem.* 266: 21911 (1991)) or recombinant human FVIIa (2 µg/ml each) were immobilized directly to **Maxisorp MaxiSorp™** plates (Nunc) in 50 mM ammonium bicarbonate, pH 9.3 by incubating overnight at 4 °C. Wells were blocked using Sorting Buffer (50 mM HEPES, pH 7.2, 5 mM CaCl₂, 5 mM MgCl₂, 150 mM NaCl, 1% BSA) for 1 h at 25 °C. Recombinant human FVIIa (2 µg/ml) in Sorting Buffer

was added for 30 min to wells previously coated and blocked with TF to form the TF-FVIIa complex. Phage from the libraries described above were pooled into 3 groups. Pool A contained $X_iCX_jCX_k$ (SEQ ID NO:103) where $j = 5 - 7$; Pool B contained $X_4CX_2GPX_4CX_4$ (SEQ ID NO:105), X_{20} (SEQ ID NO:104) and $X_iCX_jCX_k$ (SEQ ID NO:103) where $j = 4$; Pool E contained $X_iCX_jCX_k$ (SEQ ID NO:103) where $j = 8 - 10$. Phage from each pool were incubated with the immobilized targets in Sorting Buffer for 3 h at 25 °C.; generally about 5×10^{10} phage were added at the beginning of each round. Unbound phage were removed by repetitive washing with Wash Buffer (50 mM HEPES, pH 7.2, 150 mM NaCl, 0.005% Tween 20TM); remaining phage were eluted with 500 mM KCl, 10 mM HCl, pH 2. The eluted phage were then propagated in XL1-Blue cells with VCSM13 helper phage (StratageneTM) overnight at 37 °C. Enrichment could be monitored by titering the number of phage which bound to a target coated well compare to a well coated with BSA.

Please replace Table II at page 48 with the following:

Table II. Sequences Selected Using Selected Full Randomization of the A Series

SEQUENCE ID. NO.	CLONE	DEDUCED AMINO ACID SEQUENCE
<u>106</u>	Library AoN	o o X W E V X C W X W E X C X X X X X X
76	AN41	A W E V L C W A W E D C E R G A G S
77	AN33	A W E V V C W S W E T C E R G E T P
78	AN31	E W E V V C W A W E T C E R G E R Q
79	AN43	E W E V L C W E W E V C E R D I T L
80	AN42	E W E V V C W T W E A C E L G E R V
81	AN32	G W E V V C W S W E S C A R G D L E
<u>107</u>	Library AoNC	o o X W E V X C W X W E X C X o o o o o
82	ANC45	A W E V V C W S W E T C E
83	ANC41	E W E V V C W E W E N C L
84	ANC33	E W E V L C W G W E T C S
85	ANC34	G W E V L C W T W E E C S

86	ANC43	S	W	E	V	L	C	W	Q	W	E	E	C	E							
87	ANC32	T	W	E	V	L	C	W	S	W	E	S	C	E							
<u>108</u>	Library A	X	X	X	W	E	V	X	C	W	X	W	E	X	C	X	X	X	X	X	X
88	AP31	M	E	T	W	E	V	L	C	W	E	W	E	E	C	V	R	G	G	E	P
89	AP32	A	V	E	W	E	V	I	C	W	A	W	E	T	C	E	R	S	N	M	Q
90	AP33	A	V	Q	W	E	V	L	C	W	Q	W	E	N	C	H	R	G	E	Q	V
91	AP34	M	Q	G	W	E	V	V	C	W	E	W	E	G	C	A	R	G	D	H	Q
92	AP42	E	E	Q	W	E	V	V	C	W	D	W	E	T	C	D	W	P	G	K	D
93	AP43	L	G	E	W	E	V	M	C	W	T	W	E	S	C	G	W	P	V	G	S
94	AP44	M	L	D	W	E	V	V	C	W	T	W	E	S	C	V	R	E	G	K	Q
95	AP45	K	N	G	W	E	V	L	C	W	T	W	E	T	C	G	R	G	V	G	D
96	AP35	G	A	P	W	E	V	V	C	W	S	W	E	S	C	S	W	G	V	A	S
97	AP41	E	D	L	W	E	V	V	C	W	S	W	E	A	C	S	R	E	G	T	Q

- Peptide sequences were deduced from the DNA sequence of clones obtained after 4 rounds of selection.
- Shaded residues indicate the wildtype sequence which was fixed; underlined residues were fully randomized as described in text.
- "o" indicates no amino acid.